

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

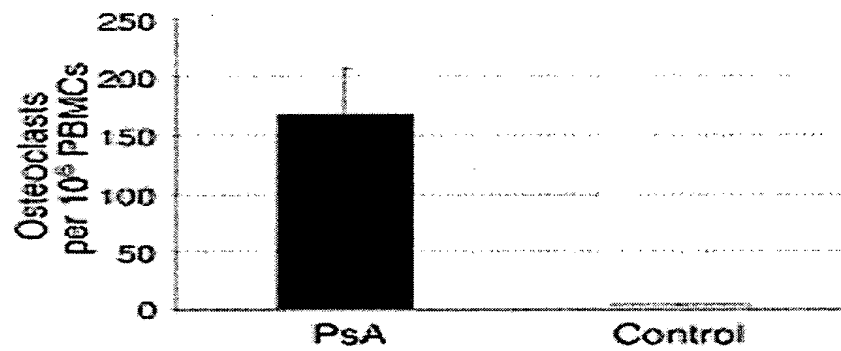


FIG. 1

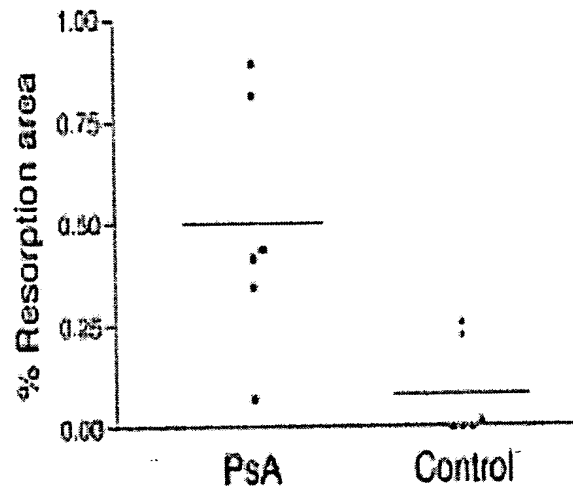


FIG. 2

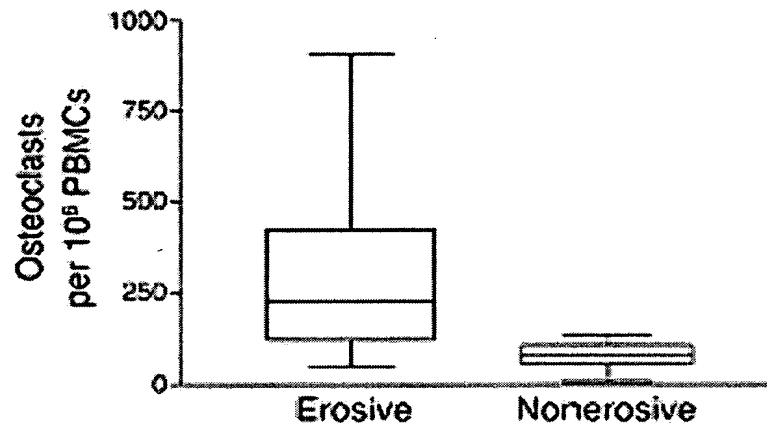


FIG. 3

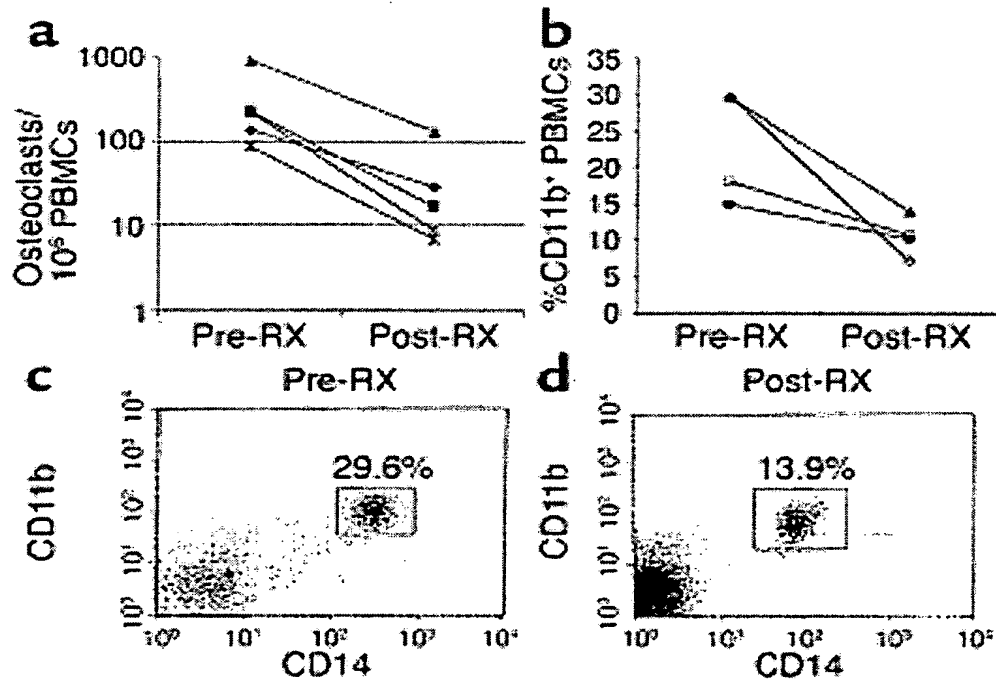


FIG. 4

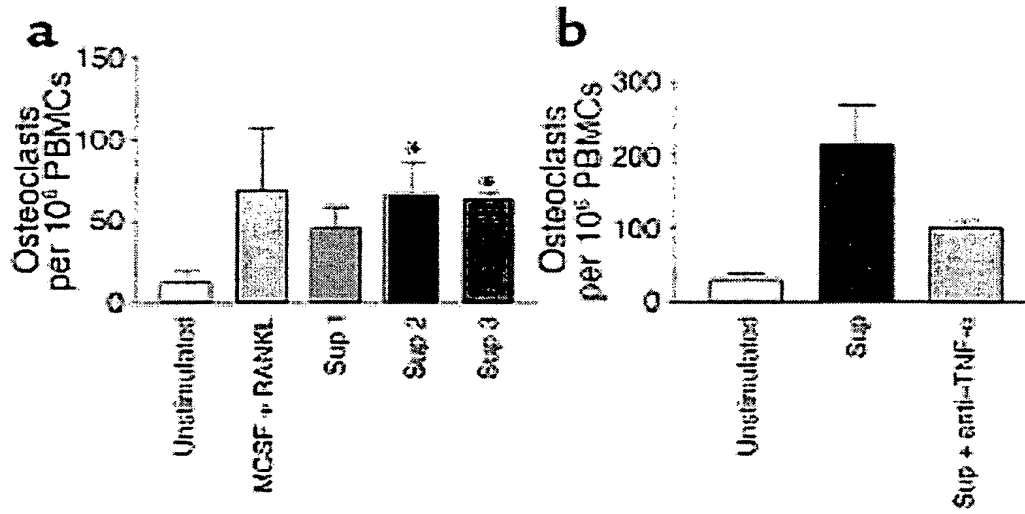


FIG. 5

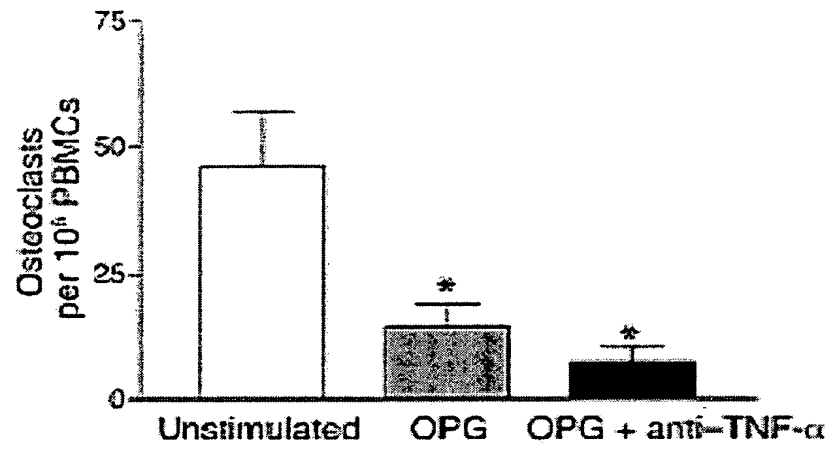


FIG. 6

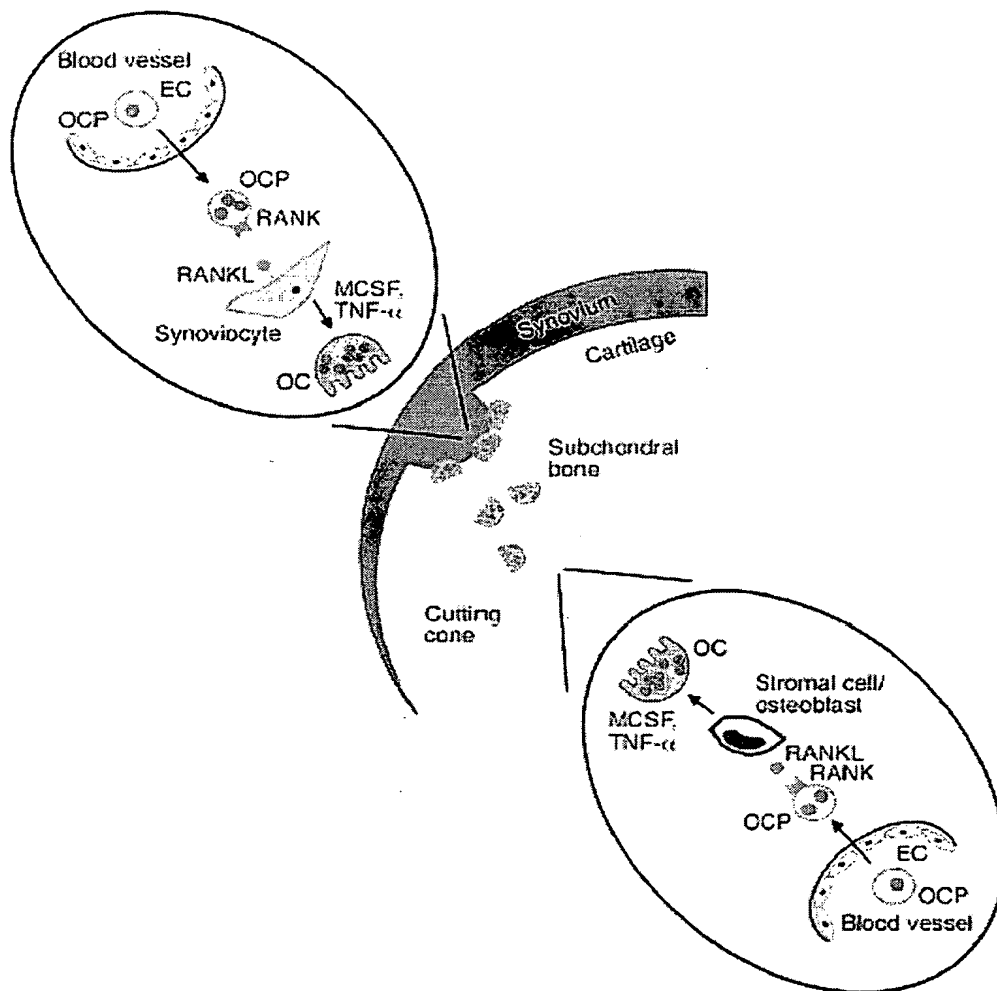


FIG. 7

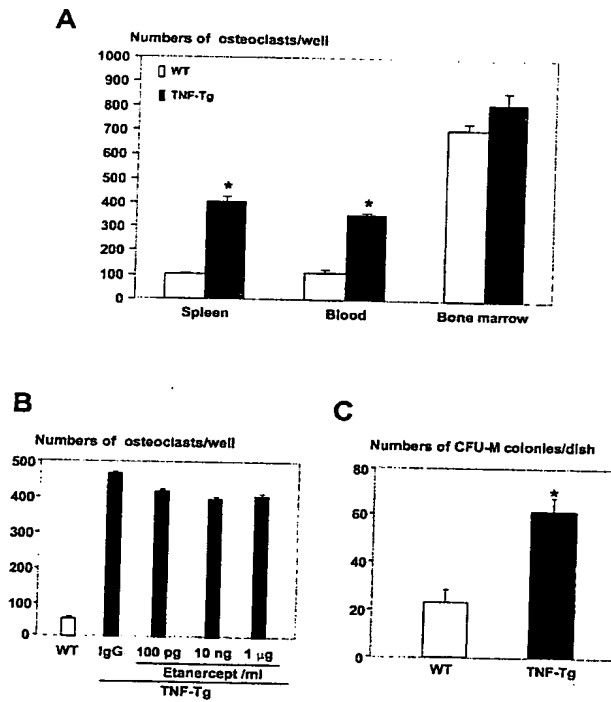


FIG. 8

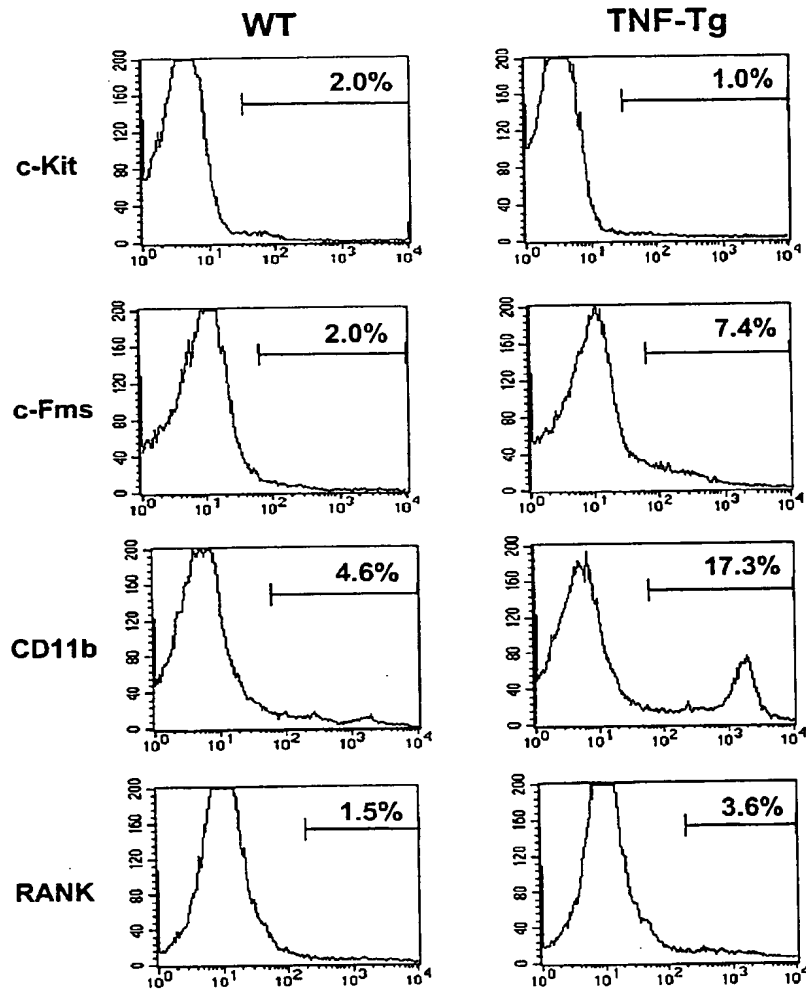
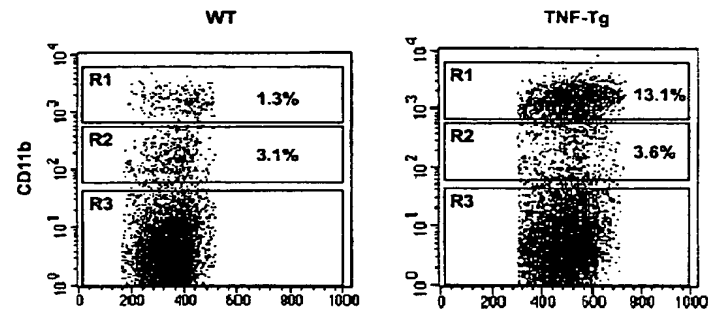


FIG. 9

A



B

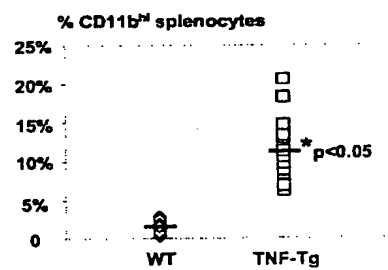


FIG. 10

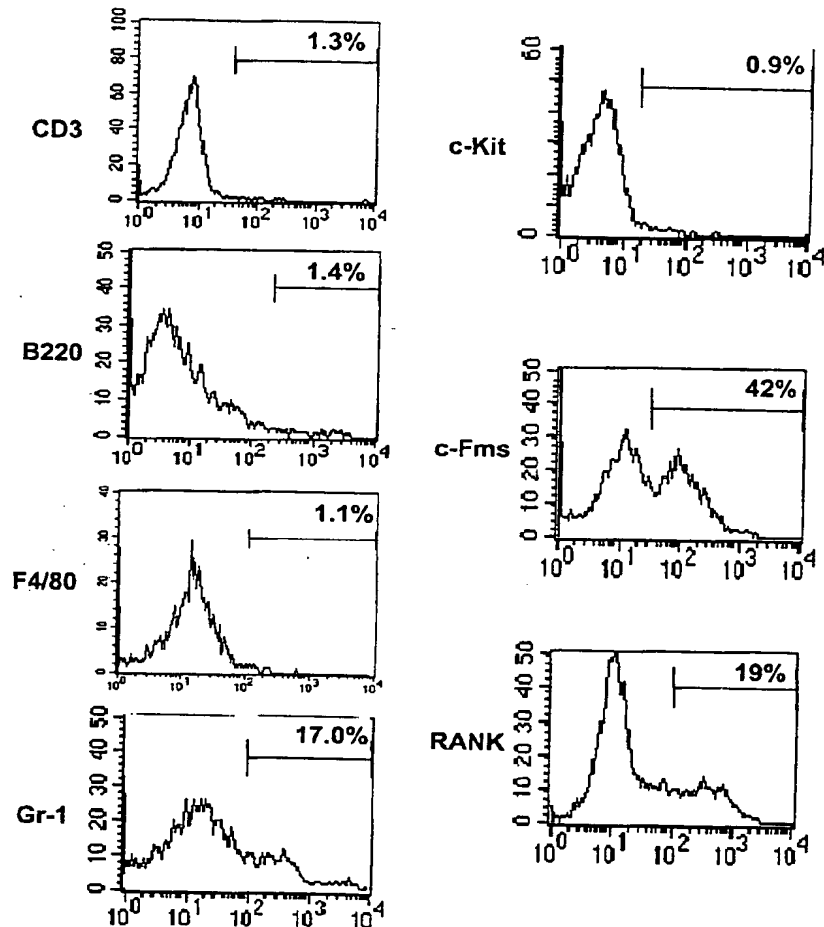


FIG. 11

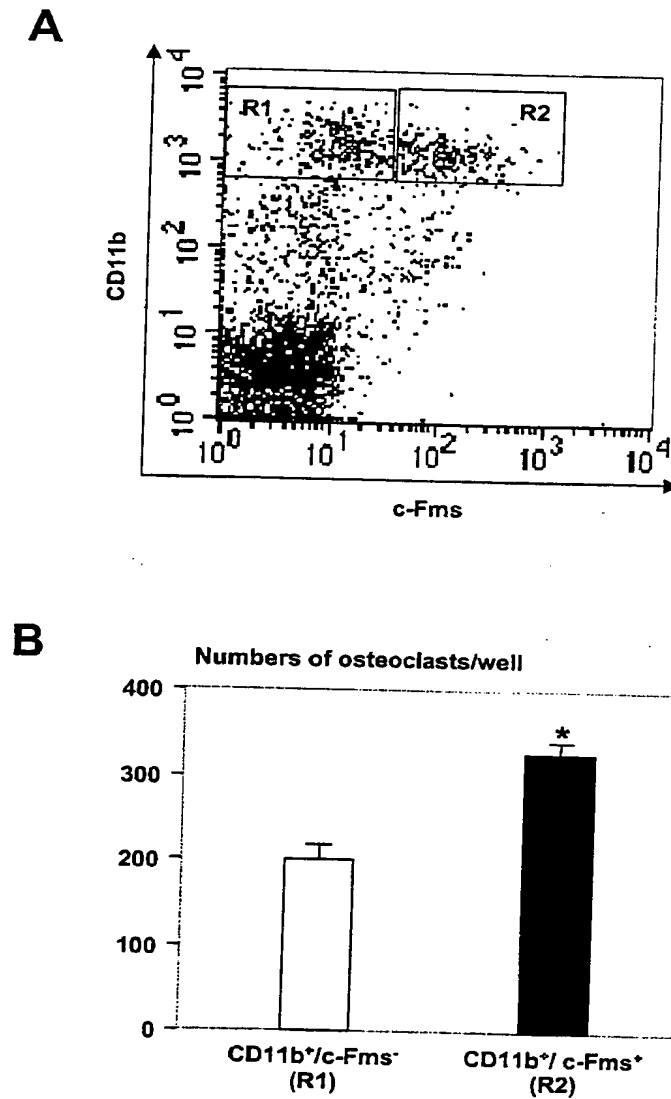


FIG. 12

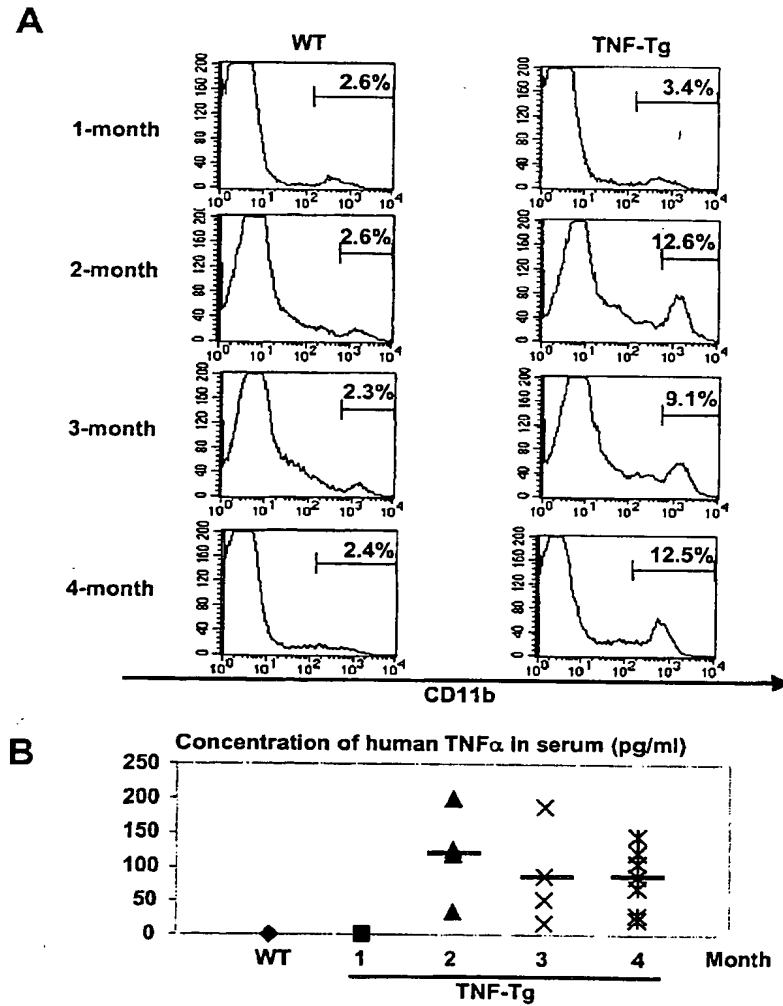


FIG. 13

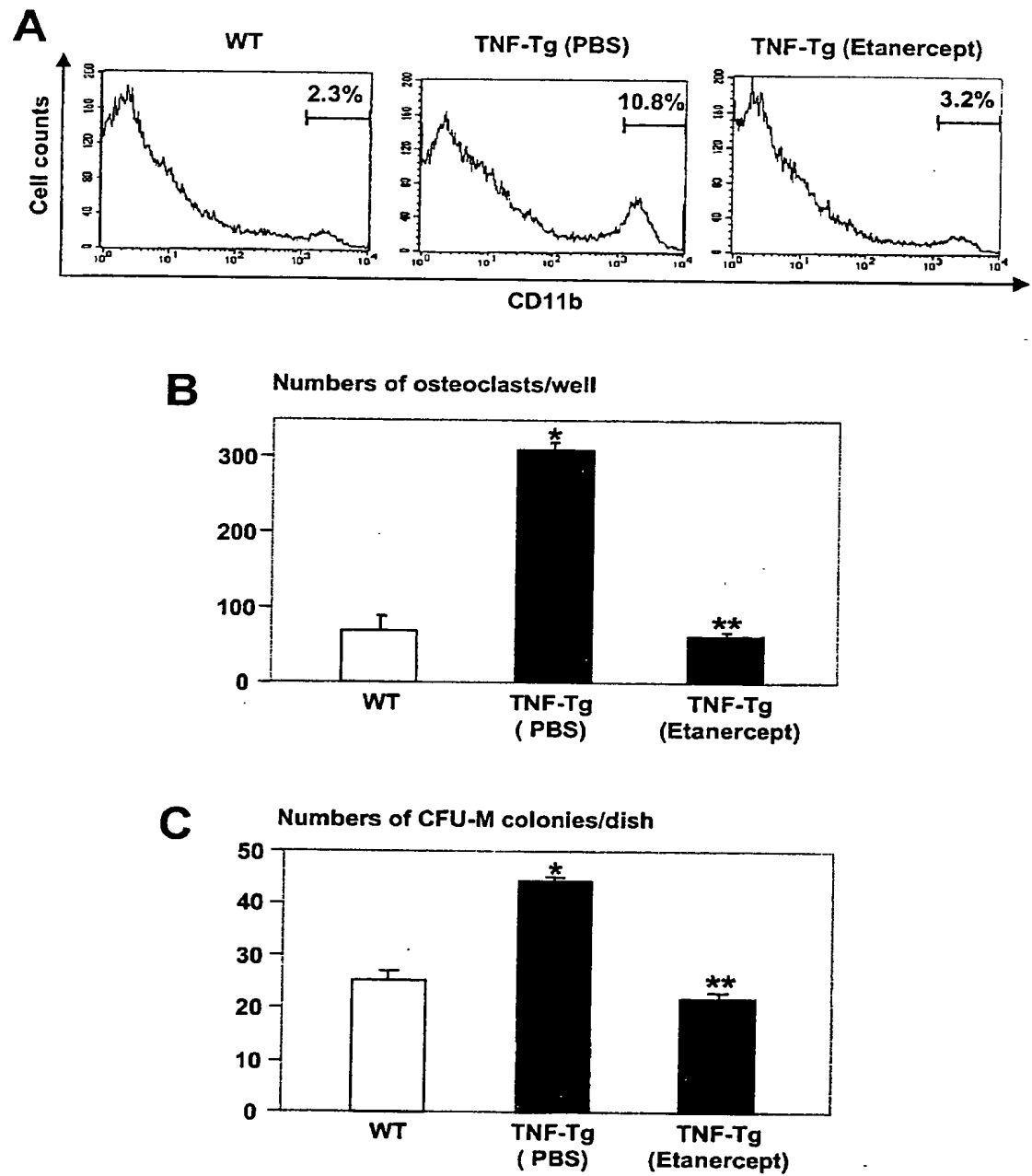


FIG. 14

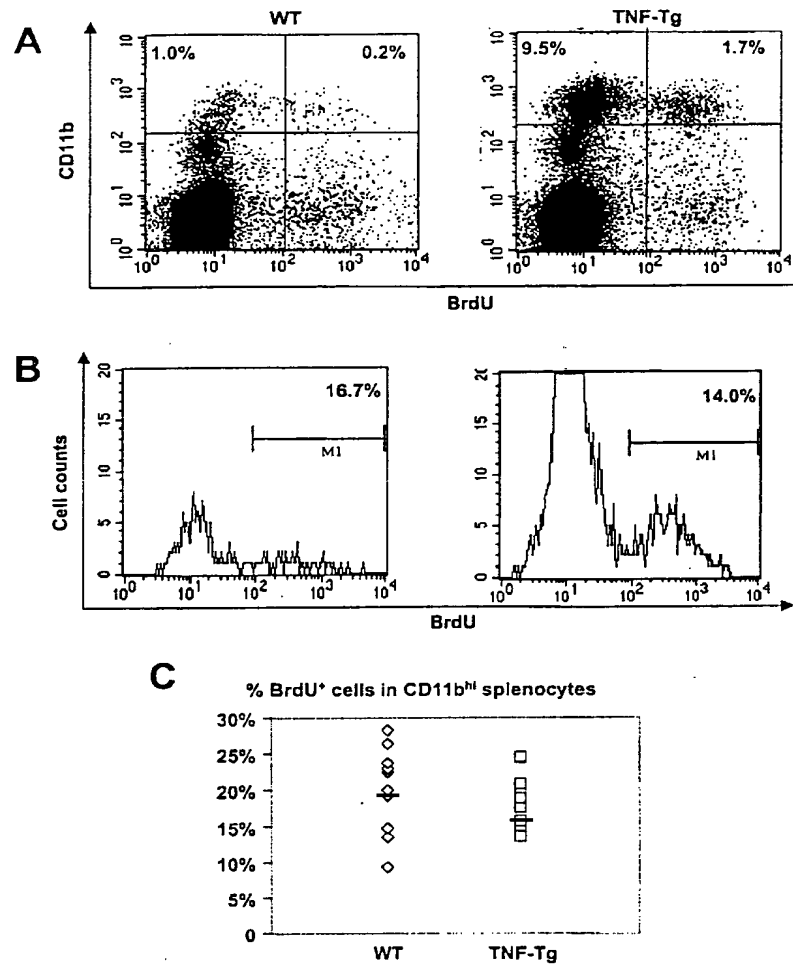


FIG. 15

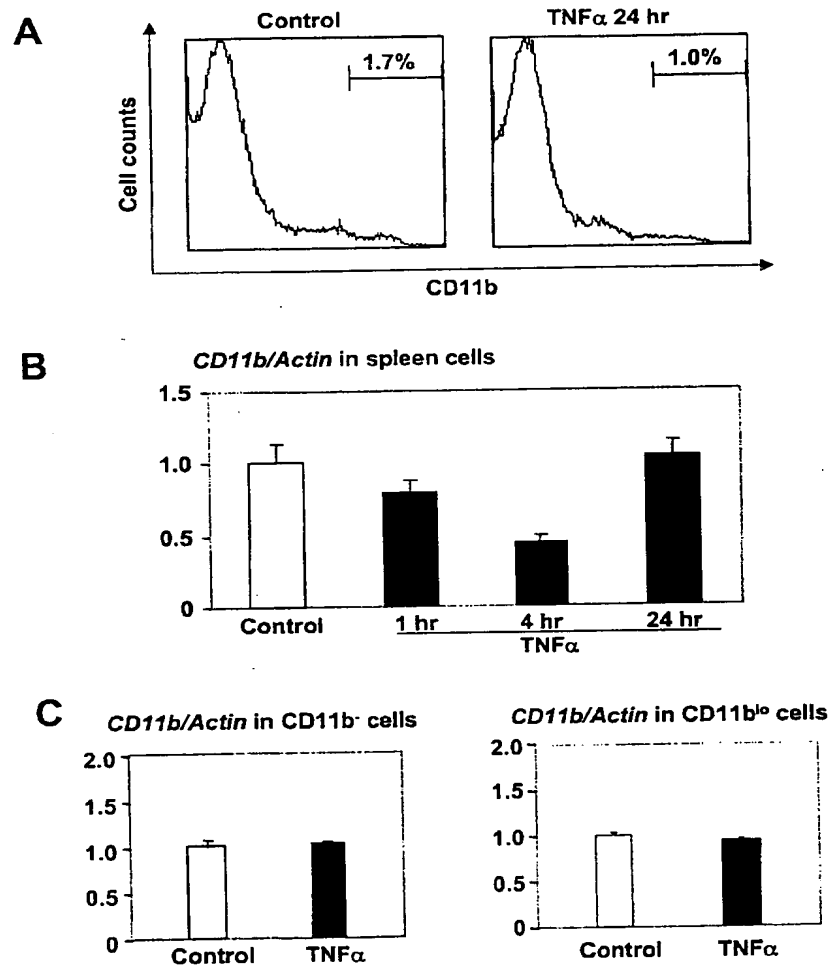


FIG. 16

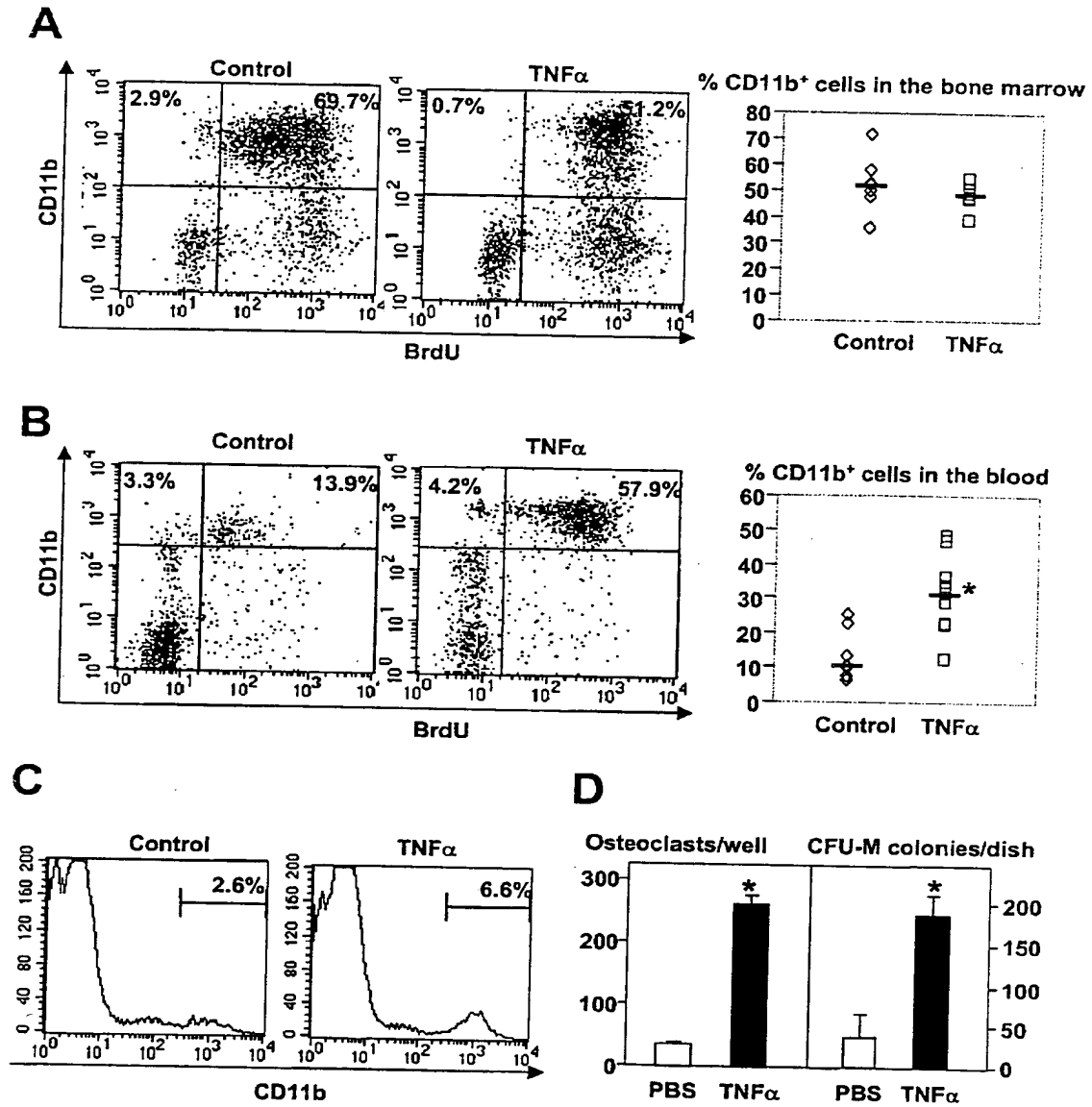


FIG. 17

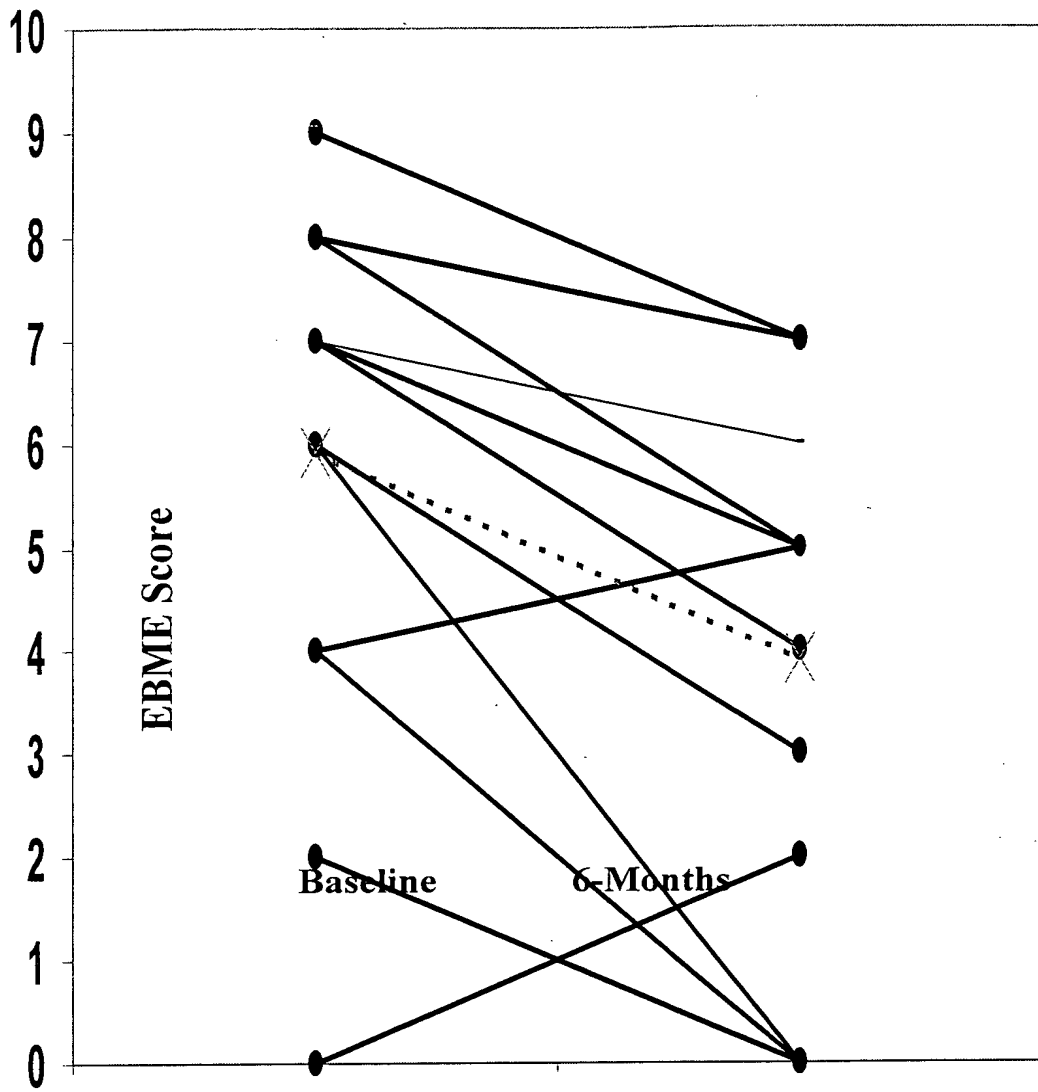


FIG. 18

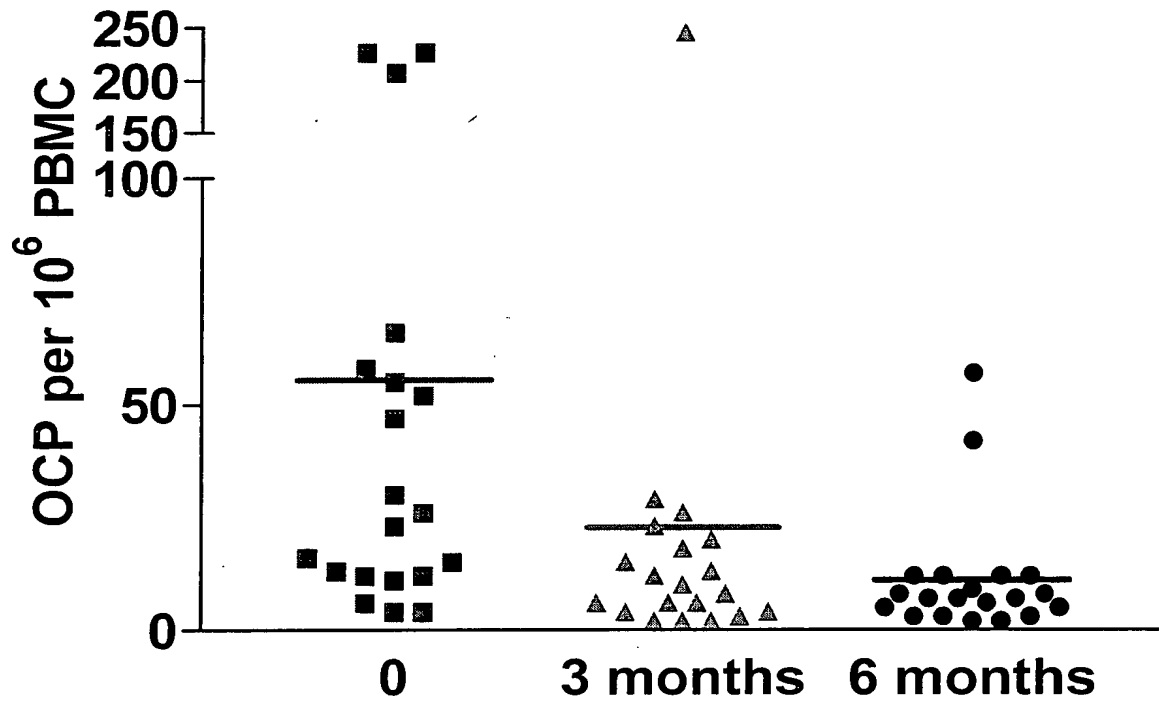


FIG. 19

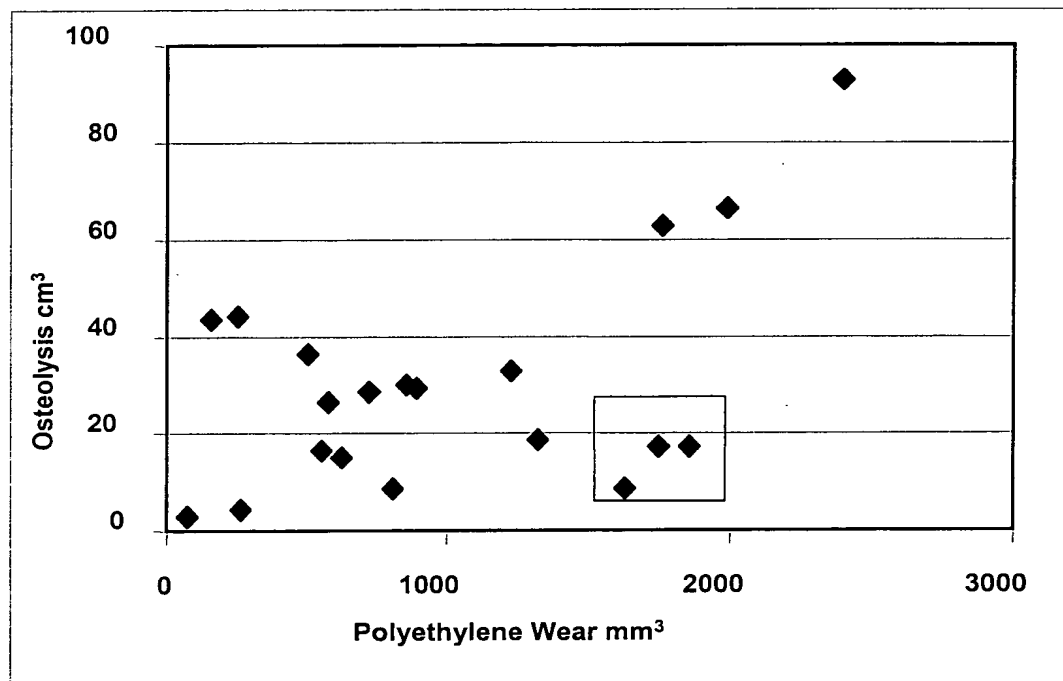


FIG. 20

clustering of 374 genes

signature

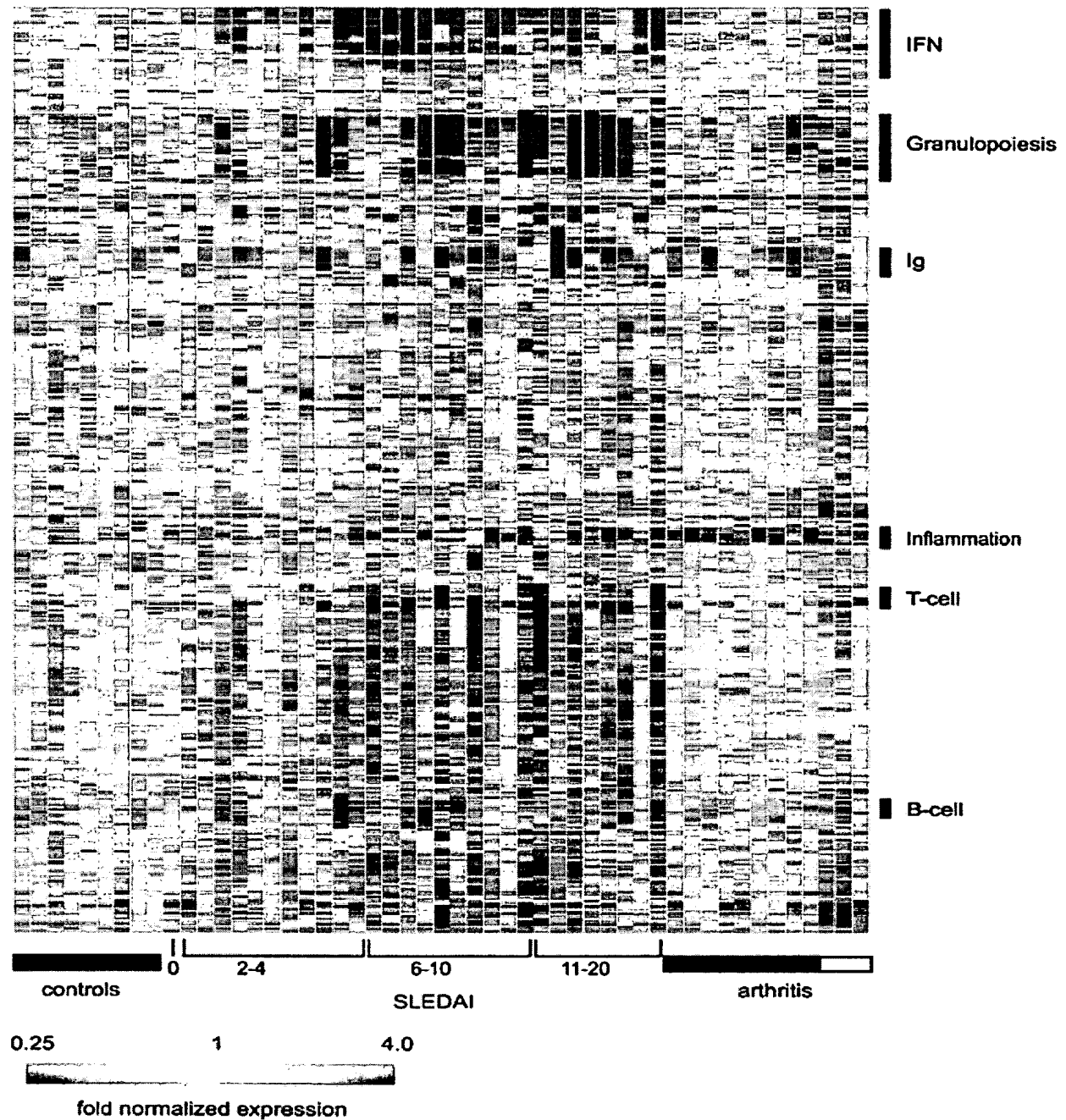


FIG. 21A

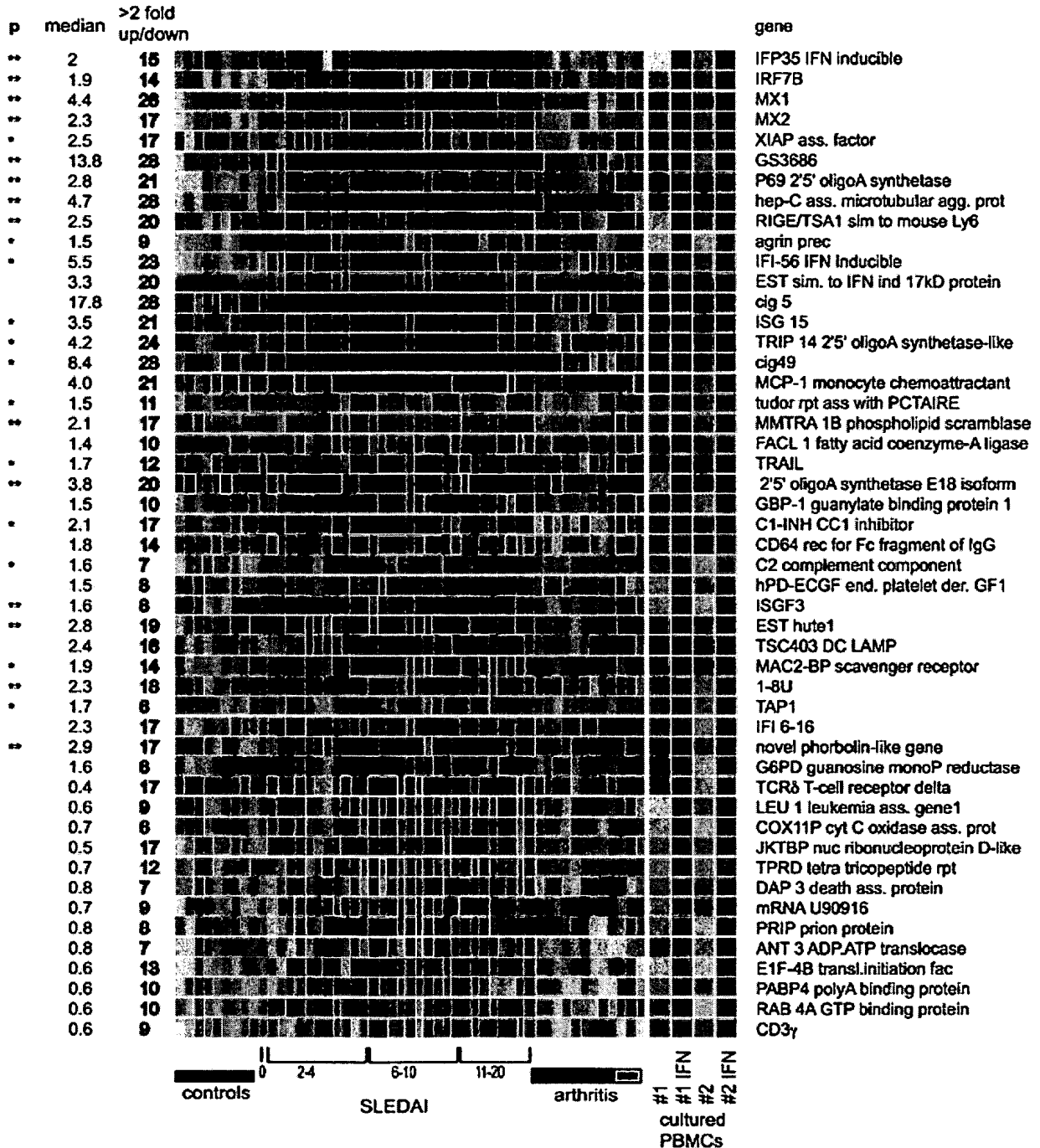


FIG. 21B

P	Gene	patient 30		patient 25		patient 5		patient 30		patient 25		patient 5	
		pre	post	pre	post	pre	post	pre	post	pre	post	pre	post
*	TRIP 14							30.0	1.0	4.2	1.0	5.7	0.6
*	IFN-ind 17kD-like							40.0	0.7	4.7	0.7	3.9	0.7
**	GS3686							25.2	0.6	16.6	1.2	14.4	1.1
*	XIAPAF-1							8.9	0.2	2.9	0.6	4.4	0.6
**	CD59							7.7	0.5	3.1	1.2	5.0	1.2
**	MX2							4.7	0.7	2.7	1.0	2.5	0.6
**	P69 OIAS							3.6	0.6	2.9	1.0	2.5	0.5
**	EST hute1							2.9	0.4	2.4	0.2	3.0	0.5
**	IRF-7							3.0	0.4	3.2	0.8	3.1	0.8
	9-27							2.8	0.4	2.3	0.3	1.9	0.8
	ISG 15							20.2	0.7	9.2	0.6	6.0	0.7
**	hep C-ass							14.5	0.7	5.2	1.3	4.2	1.1
**	MX1							10.0	0.3	9.2	0.9	6.9	0.6
*	IFI 56							70.0	0.9	10.2	1.2	6.7	0.8
*	cig 49							70.7	0.7	13.6	1.1	12.2	1.3
*	MCP-1							70.5	2.5	6.3	3.0	8.8	1.4
								p=0.002		p=0.0002		p<0.0001	
**	DEF3							4.6	10.8	15.4	6.7		
*	RNS2							2.9	3.6	7.4	3.8		
*	DEFA1							6.8	43.5	35.8	3.0		
*	FALL39							4.5	38.0	9.7	1.0		
*	sim to calgranulin							2.4	3.0	3.3	3.0		
*	F2RPA							4.1	1.6	2.9	5.0		
								p=0.14		p=0.15			

FIG. 21C

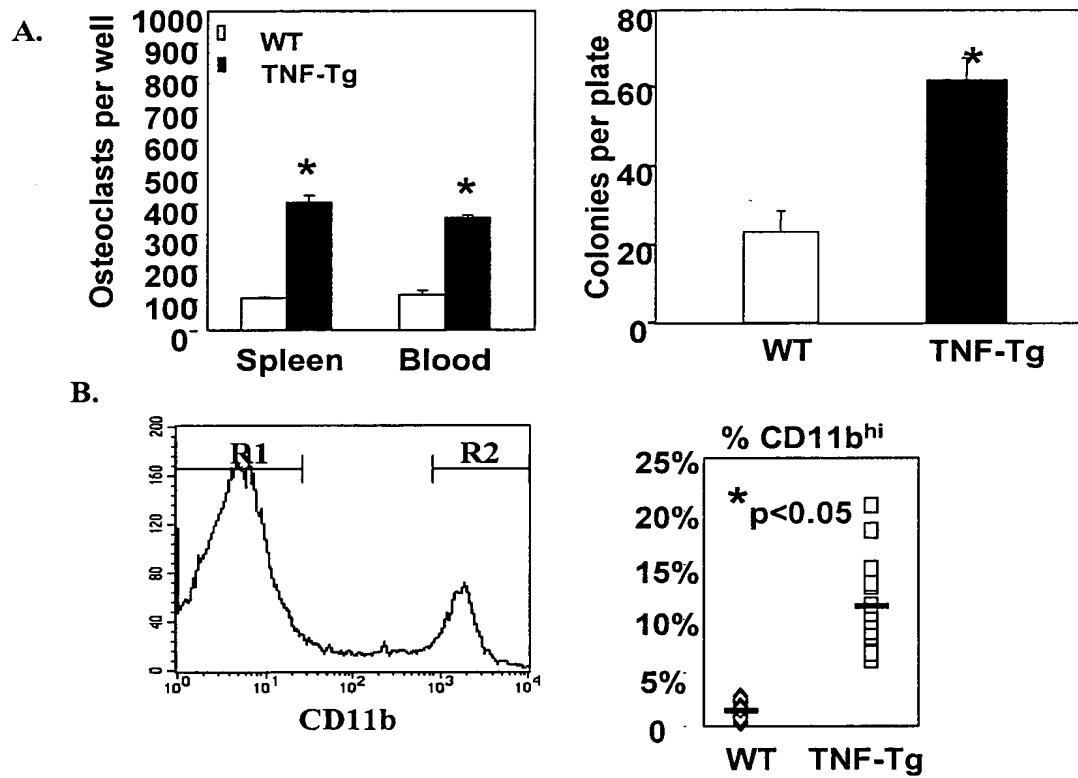


FIG. 22

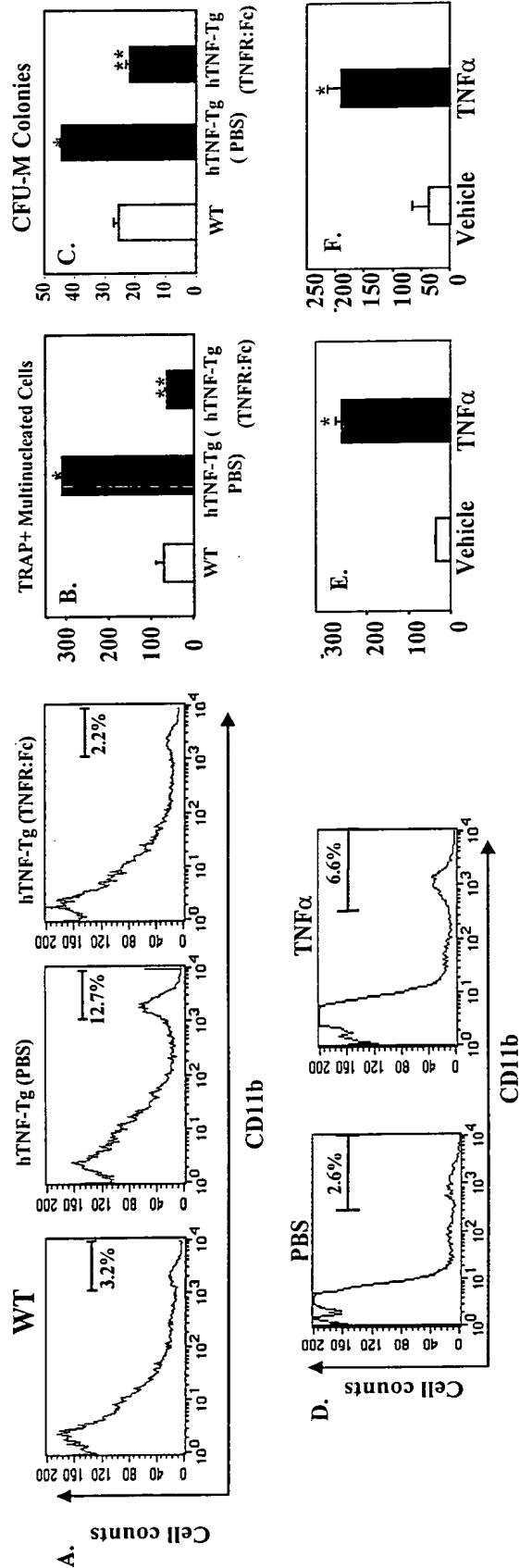


FIG. 23

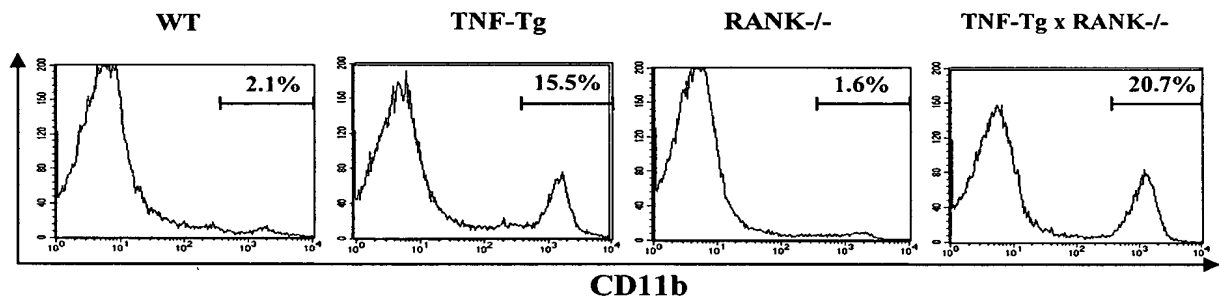


FIG. 24

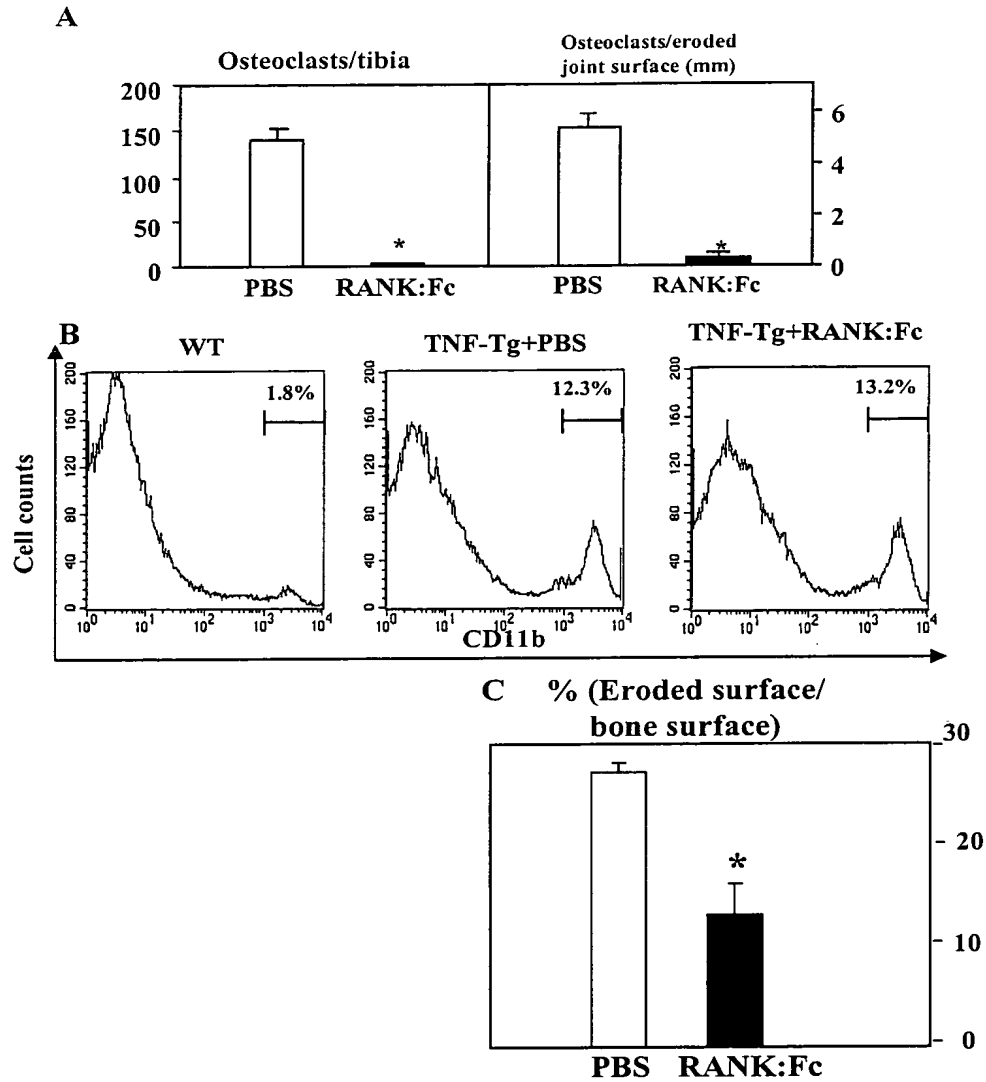


FIG. 25

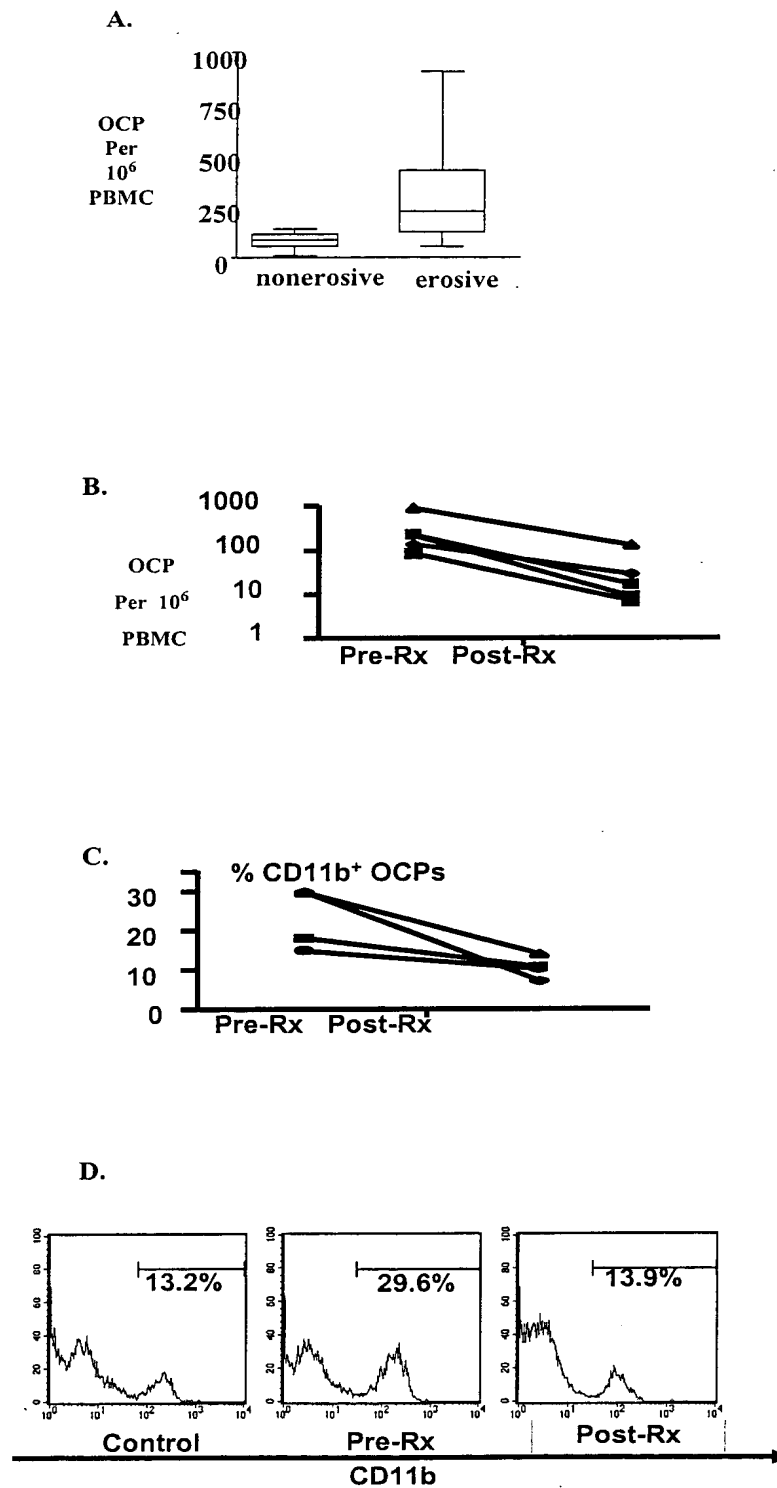


FIG. 26

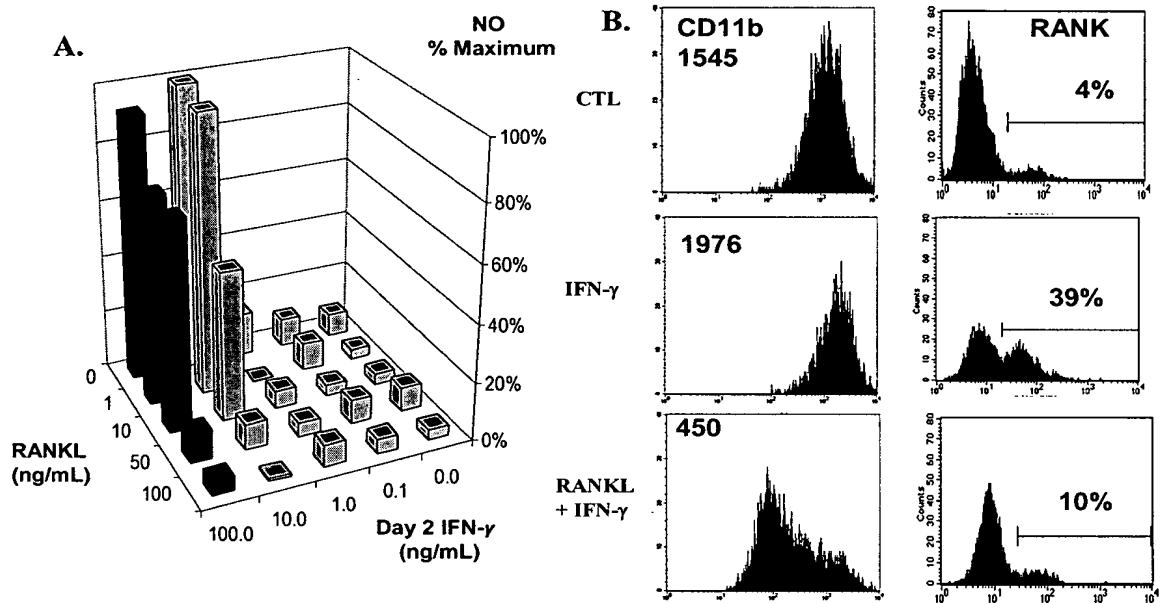


FIG. 27

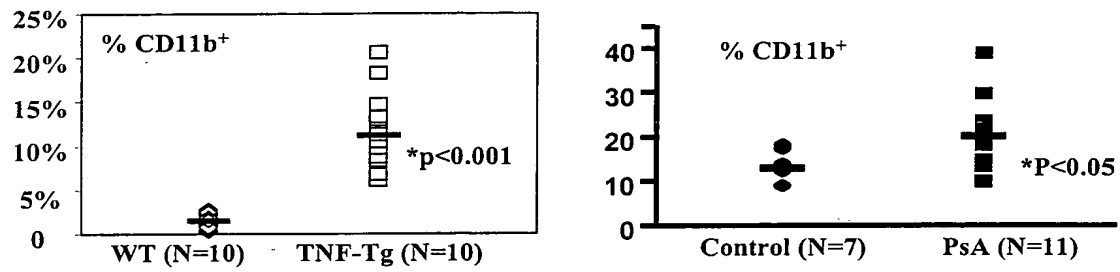


FIG. 28

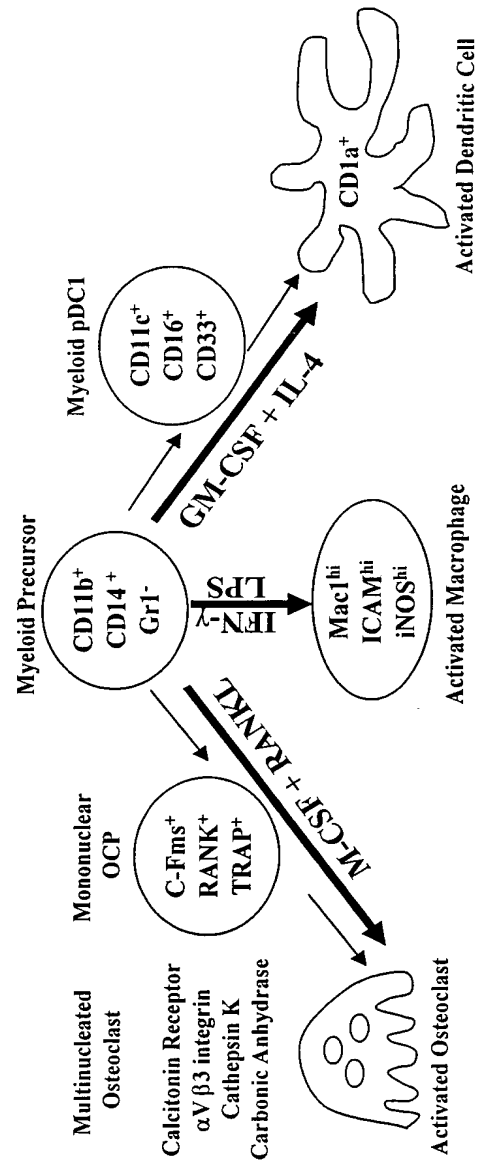


FIG. 29

clustering of 374 genes

signature

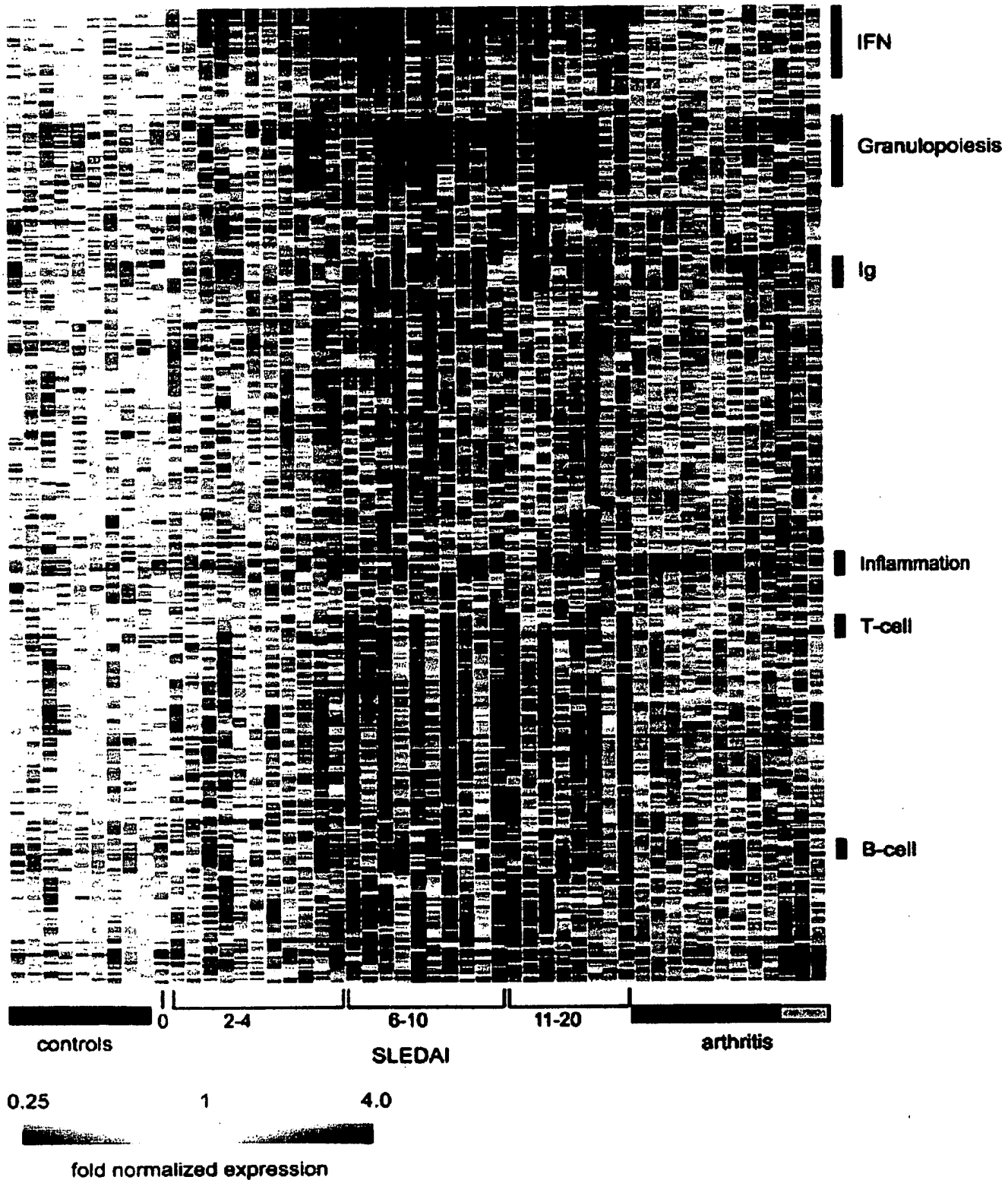


FIG. 30A

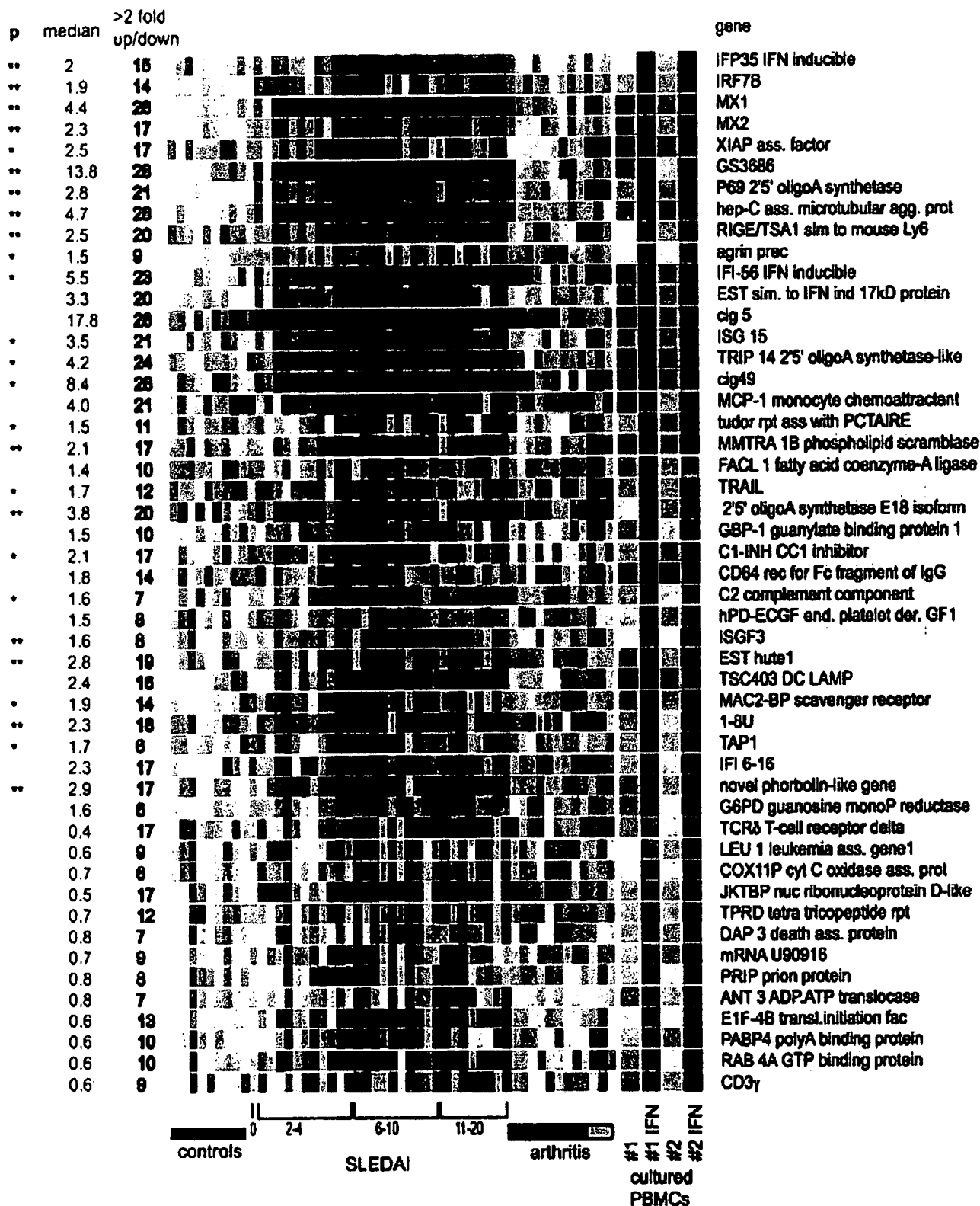


FIG. 30B

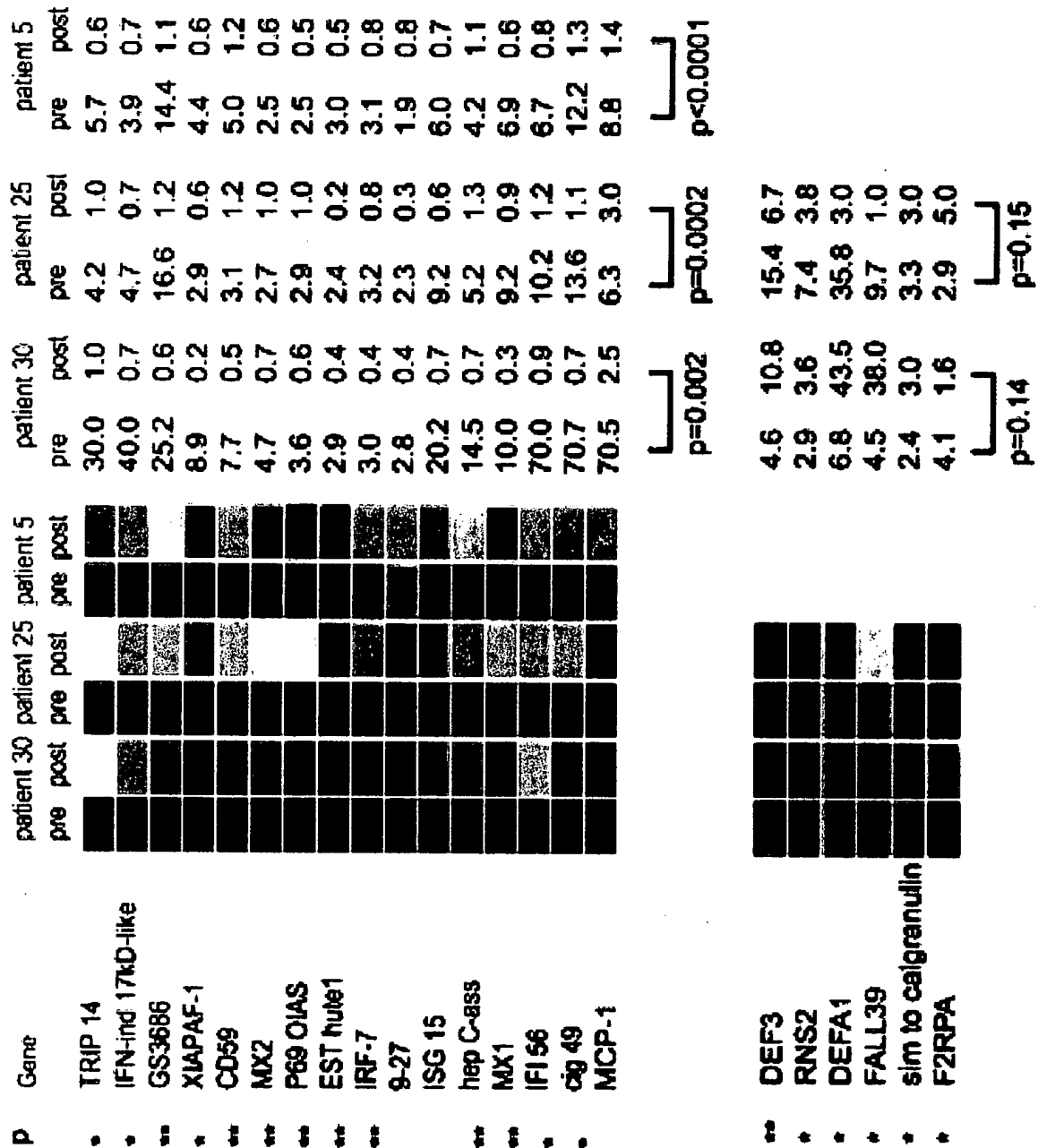


FIG. 30C